

Applicant: Rajasekhar Bandaru
Title: 68730 and 69112, Protein Kinase Molecules and
Ther
Attorney/Agent: Jill Uhl
Docket No.: MPI2000-521P1R(M)
Sheet 1 of 8 Sheets

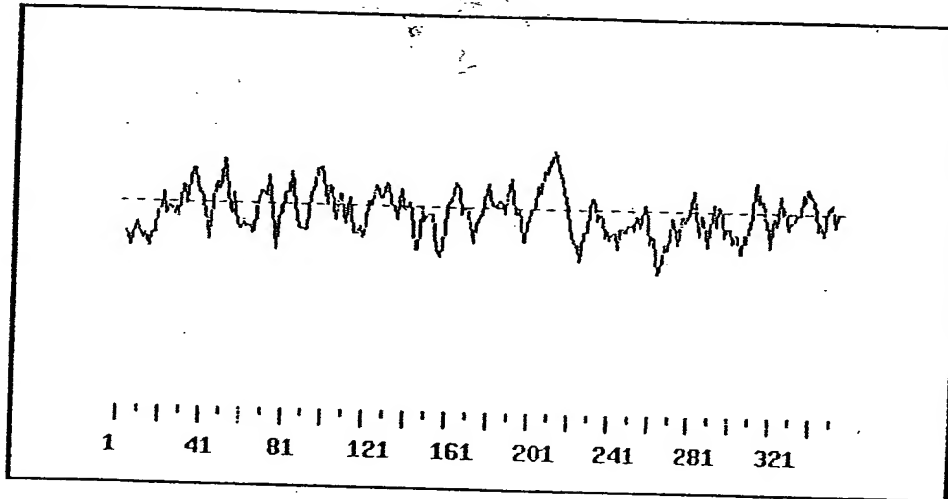


FIGURE 1

Applicant: Rajasekhar Bandaru

Title: 687 [redacted] d 69112, Protein Kinase Molecules and Uses
Therefor

Attorney/Agent: Jill Uhl

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Sheet 2 of 8 Sheets

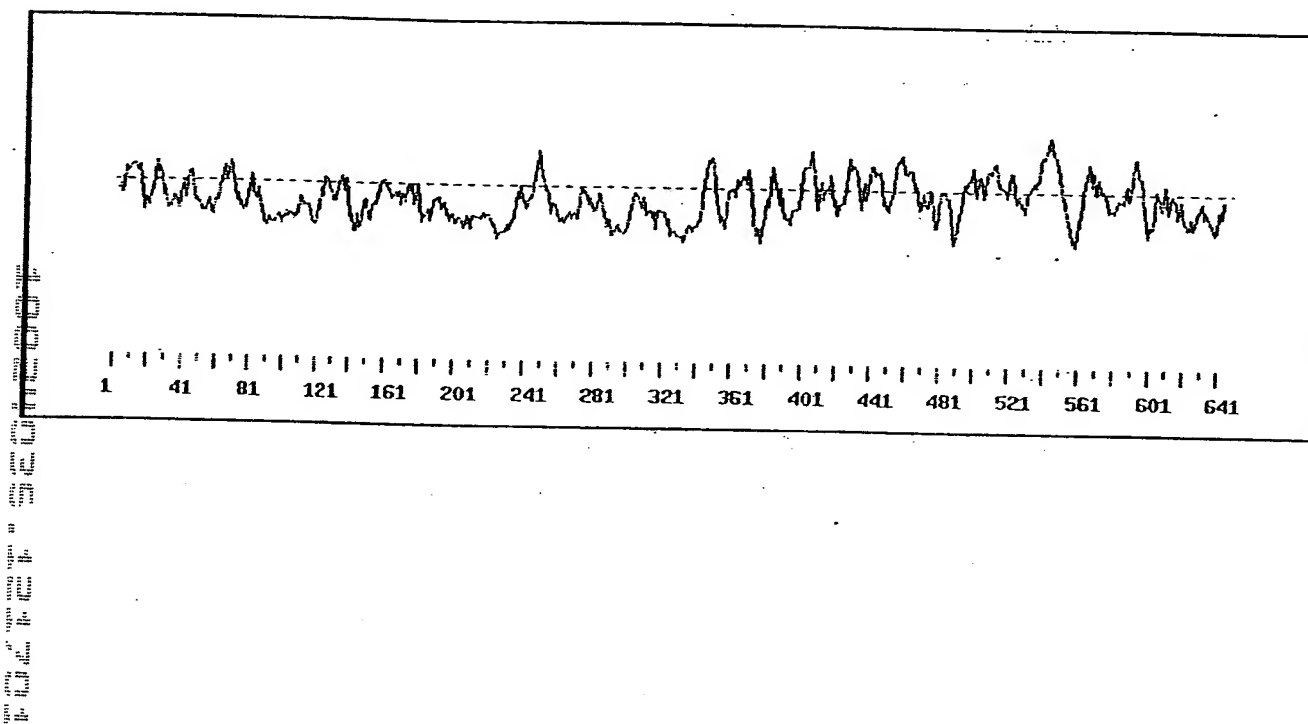


FIGURE 2

pkinese: domain 1 of 1, from 23 to 279: score 346.3, E = 3.4e-100
 *->yelleklGeGsfgkVykakhk.tgkivAvKilkkesls.....lrE
 +e++e+lG G+f++V +a++k tgk++AvK+++k+ l+++++ +E
 68730 23 FEFKETLGTGAFSEVVLAEKaTGKLFaVKCIPKKALKgkessiENE 69
 iqilkrllsHpNIvrllgvfedtddhlylvmEymegGdLfdylrrngplse
 i++l++++H+Niv l +++e +++hlylvm+++ gG+Lfd++++g ++e
 68730 70 IAVLRKIKHENIVALEDIYE-SPNHLYLVMQLVSGGELFDRIVEKGFYTE 118
 keakkialQilrGleYlHsngivHRDLKpeNILlden...gtvKiaDFGL
 k+a +++Q+l ++ YLH++givHRDLKpeN+L +++++ ++ i+DFGL
 68730 119 KDASTLIROVLDAVYYLHRMGIVHRDLKPENLLYYSQdeeSKIMISDFGL 168
 Arll...eklttfvGTpwYmmAPEvilegrgysskvDvWSlGviLyEllt
 ++ +++ +++++ +GTP+Y+ APEv l +++ys++vD WS+Gvi y ll+
 68730 169 SKMEgkgDVMSTACGTPGYV-APEV-LAQKPYSKAVDCWSIGVIAIYILLC 216
 ggplfpgadlpafgtggdevdqliifvklPfsdelpktridpleelfrik
 g +Pf+d ++ ++lf+ +
 68730 217 G-----YPPFYD-----ENDSKLFEQI 233
 kr.....rlplpsncSeelkdLlkkcLnkDPskRpGsatakeilnhpwf<
 ++ + + +p ++ +S+++kd+++ + +kDP+kR+ t++++ hpw+
 68730 234 LKaeyefDSPYWDDISDSAKDFIRNLMEKDPNKRY---TCEQAARHPWI 279
 -*

FIGURE 3A

$\frac{d}{dt} \left(\frac{\partial L}{\partial v} \right) = \frac{\partial L}{\partial x}$

FIGURE 3B

tyrkin_6: domain 1 of 1, from 23 to 279: score 35.7, E = 4e-14
 *->ltlgkklGeGaFGeVykgtlk...ieVAVKtLkeda....keeflrE
 +++++LG GaF eV++++ k ++ AVK++ + a +++++ + +E
 68730 23 FEFKETLGTGAFSEVLAEEKatqKLEAVKCI PKKalkgkESSIENE 69
 akiMkklGgkHpNiVklLlGvcteeegrrFmevePlmivmEymegGdLldyL
 + +++k+ kh+NiV+L + ++ l++vm +++gG L d++
 68730 70 IAVLRKI--KHENIVALEDIYESP-----NHLYLVMLVSGGELFDRI 110
 rknpklsldLlsfAlQIAkGMeYLesknfvHRDLAARNcLvgenk...
 ++ + +d Q+ + YL++++vHRDL N L+ ++ +++
 68730 111 -VEKGFYTEKDASTLIROVLDAVYYLHRMGIVHRDLKPENLLYYSDDees 159
 vvKISDFGLsRdlyddDkkGeskdYrkkggkgtllPirWmAPeslkd
 + IsDFGLs+ + + d+ +++ g+ + APE+l
 68730 160 KIMISDFGLSKMEGKG-----DVMSTAC--GTPG-----YVAPEVLAQ 195
 gkFtskSDVWSFGVLWEiftlGegPYpgeiqqfmsneevleylkkGyRl
 + ++ + D WS GV + i+ G +P ++ +++ ++e++ k ++
 68730 196 KPYSKAVDCWSIGVIAY-ILLCGYPPFYD-----ENDSKLFEQILKAEYE 239
 pkPendlpiSs....vtCPdelydlMlqCwaedPedRPtFsel..verl<
 ++ ++ + + d + +lM++ dP++R t ++ ++ +
 68730 240 FDSPY-----WddisDSAKDFIRNLMEK----DPNKRYTCEQAarHPWI 279

FIGURE 3C

pkinase: domain 1 of 1, from 356 to 613: score 350.2, E = 2.3e-101

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*->yelleklGeGsfgkVykakhk.tgkivAvKilkkesls.....lrE
ye+f+++G G+f++V+++h+++ + +A+Ki++k++l++++ +E
69112 356 YETGRVIGDGNFAVVKECRHReTRQAYAMKIIDKSRLKgedmvdSE 402

iqilkrIshpNIvrlIlgvfedtdhlylvmEymegGdLfdylrrngplse
i i ++lshpNIv+l++v+e td ++yl++Ey+ gGdLfd + + +++e
69112 403 ILIIQSLSHpNIvKLHEVYE-TDMEIYLILEYVQGGDLFDAIESVKFPE 451

keakkialQilrGleYlHsngivHRDLKpenILlden....gtvKiaDFG
++a ++ +++++l ++H+++ivHRDLKpen+L+ +n++++ t+K+aDFG
69112 452 PDAALMIMDLCKALVHMHDKSIvHRDLKpenLLVQrNedksTTLKLADFG 501

LArll.eklttfvGTpwYmmAPEvilegrgysskvDvWSlGvilyElltg
LA+ + + t++GTP+Y+ APE+ l+ +gy+ +vD+W+ Gvily ll+g
69112 502 LAKHVvRPIFTVCGTPTYV-APEI-LSEKGYGLEVDMWAAGVILYILLCG 549

gplfpgadlpaftggdevdqliifvklPfsdelpktridpleelfrikk
+Pf+ ++ +elf+i++
69112 550 -----FPPFRS-----PERDQDELFNIIQ 568

r.....rlplpsncSeelkdLlkkcLnkDPskRpGsatakeilnhpwf<-
++ + ++p ++n+S+++kdL++++L +DP+kR+ ta+++l+hpw+
69112 569 LghfeFLPPYWDNISDAAKDLVSRLLVVDPKKRY---TAHQVLQHPWI 613
  
```

FIGURE 4A

serkin_6: domain 1 of 1, from 356 to 613: score 372.7, E = 3.8e-108
 *->YellkklGkGaFGkVylardkktgrlvAiKvik.....erilrE
 Ye ++++G G F++V+ +r+++t + +A+K+i++++ ++++++ +E
 69112 356 YETGRVIGDGNFAVVKECRHRETRQAYAMKIIDksrlkgkeDMVDSE 402
 ikiLkk.dHPNIVkLydvfed.dklylVmEyceGdlGdLfdllkkrgrg
 i i ++ HPNIVkL++v+e++ ++yl++Ey+ G GdLfd + + +
 69112 403 ILIIQSLSHPNIVKLHEVYETdMEIYLILEYVQG--GDLFDAIIESVK-- 448
 lrkvlsE.earfyfrQilsaLeYLHsqgIiHRDLKPeNiLLds.....h
 ++E++a+ ++ +++aL ++H++ I+HRDLKPeN+L+ +++++++
 69112 449 ----FPEpDAALMIMDLCKALVHMHDKSI[↑]VHRDLKPENLLVQRnedkstT[↑] 494
 vKlaDFGlaArql....ttfvGTpeYmAPEvl...gYgkpavDiWSlGcil
 +KlaDFGla+++ ++ t++GTP Y+APE+l+++gYg +vD+W+ G+il
 69112 495 LKLADFGlAKHVvrpiFTVCGTPTYVAPEILsekGYGL-EVDMWAAGVIL 543
 yElltGkpPFp....qldlifkkig.....SpeakdLikkl
 y+ll+G pPF+++++++d++f++i ++ + ++++++ S+ akdL+++l
 69112 544 YILLCGFPPFRsperDQELFNIIQlghfeflppywdniSDAAKDLVSRL 593
 LvkdPekRlta.eaLedeldikaHPff<-*
 Lv+dP+kR+ta+++L+ HP++
 69112 594 LVVDPKKRYTAhQVLQ-----HPWI 613

FIGURE 4B

tyrkin_6: domain 1 of 1, from 356 to 613: score 50.0, E = 5.3e-15
 *->ltlgkklGeGaFGeVykgtlk...ieVAVKtLkeda...keeFlrE
 + g+++G G+F +V +++ +++++ A K + ++ +++++ + +E
 69112 356 YETGRVIGDGNFAVVKECRHRetrQAYAMKIIDKSRLkgkEDMVDSE 402
 akimkklGgkHpNiVklLlGvcteegrrfmevePlmivmEymegGdLldyl
 + i +l +HpNiVkl+ v ++ +++++Ey+ gGdL d +
 69112 403 ILIIQSL--SHPNIVKLHEVYETD-----MEIYLILEYVQGGDLFDAI 443
 rknrpklslsdLlsfAlQIAkGMeYLesknfvHRDLAARNcLvgenk...
 ++ + ++ +d + + +k + ++k +vHRDL N Lv +n +++
 69112 444 IESVK-FPEPDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNEdks 492
 .vvKIsDFGLsRdlyddDkkGeskdYrkkggkggkllPirWmAPESlk
 ++ K +DFGL++ + ++ +g APE l
 69112 493 tTLKLADFGGLAKHVVRP-----IFTV----CGTP----TYVAPEILS 526
 dgkFtskSDVWSFGVllWEiftlGeqPYpgeiqqfmsneevleylkkGyR
 ++ + + D W+ GV L+ i+ G +P ++ + +e+++ ++ G+
 69112 527 EKGYLEVDMWAAGVILY-ILLCGFPPFRSPE---RDQDELFNIIQLGHF 572
 lpkPendlpisSvtCPdelydlMlqCwaedPedRptFsel..verl<-*
 P++ +d+ dl ++ dP++R t ++ ++ +
 69112 573 EFLPPY-----WDNISDAAKDLVSRLLVVDPKKRYTAHQVlqHPWI 613

FIGURE 4C